

OM nucleic - nucleic search, using sw model

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Run on:      March 20, 2003, 01:47:25 ; Search time 237 Seconds
              (without alignments)
              5311.675 Million cell updates/sec
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Title: US-09-867-958-2
Perfect score: 500

Sequence: 1 ccgcacatgacacgcgcacac.....cgctagaccttgcacgcg 559

Scoring table: IDENTITY_NUC

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N_Geneseq_101002:*

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23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT *
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT *

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	559	100.0		559	20	AAK36136	DNA encoding a hum
	2	549.4	98.3		1006	22	AA158712	Human polynucleoti
	3	434.4	77.7		1859	22	AAK55488	Human immune/haema
	4	432.2	77.3		1869	22	AA158813	Human polynucleoti
	5	381.8	68.3		1074	22	AA160498	Human polynucleoti
	6	103	18.4		2007	24	ABO54845	Human ovarian anti
	7	102.6	18.4		764	22	AA197619	Human neuroblastom
	8	101.2	18.1		483	22	AAH41100	Nucleotide sequenc
	9	94.2	16.9		569	24	ABQ59935	Human colon cancer

C 10	94.2	16.9	664	24	ABO57521	Human colon cancer
C 11	93	16.6	570	24	AB137927	Human colon tumour
C 12	84.4	15.1	575	24	ABO59145	Human colon cancer
C 13	82.6	14.8	561	24	ABO58116	Human colon cancer
C 14	75.2	13.5	473	24	ABK09599	Human ovarian tumo
C 15	65.4	11.7	418	24	ABN858218	Human colon cancer
C 16	56.6	10.1	1776	24	ABL136964	Human NS cDNA sequ
C 17	54.4	9.7	314	22	AAFG4993	Nucleic acid sequen
C 18	50.4	9.0	477	21	AAFG1984	Human breast and o
C 19	48.8	8.7	447	22	AA1E2544	Human polynucleoti
C 20	45.2	8.1	587	21	AAVC06233	Human secreted pro
C 21	39	7.0	441	23	ABV17722	Human prostate exp
C 22	39	7.0	497	23	ABV47515	Human prostate exp
C 23	38.2	6.8	2418	23	ABL03387	Drosophila melanog
C 24	38.2	6.8	4204	23	ABL04654	Drosophila melanog
C 25	38.2	6.8	4477	23	ABL03386	CDNA encoding huma
C 26	35.2	6.3	301	24	ABK93035	CDNA encoding novel
C 27	35.2	6.3	3929	23	AA570024	Human mucosal
C 28	35.2	6.3	3933	16	AA1O3885	Human foetal
C 29	34.6	6.2	467	22	ABAF1936	Probe #217 for
C 30	34.6	6.2	467	22	ABAF1751	Human brain exp
C 31	34.6	6.2	467	22	AAK00225	Human bone marrow
C 32	34.6	6.2	467	22	AAK5668	Probe #228 for gen
C 33	34.6	6.2	467	22	AA110295	Probe #230 used to
C 34	34.6	6.2	467	22	AA11544	Probe #222 used to
C 35	34.6	6.2	467	22	AA100231	Human genome-deriv
C 36	34.6	6.2	467	24	AB5006240	Human foetal cell
C 37	34.6	6.2	1186	22	ABBA66719	Human foetal liver
C 38	34.6	6.2	1186	22	ABBA64555	Probe #10187 for g
C 39	34.6	6.2	1186	22	AAK131721	Human brain expres
C 40	34.6	6.2	1186	22	AAK13036	Human bone marrow
C 41	34.6	6.2	1186	22	AAK38767	Probe #9506 for ge
C 42	34.6	6.2	1186	22	AA119573	Probe #13451 used
C 43	34.6	6.2	1186	22	AA1474765	Probe #5284 used t
C 44	34.6	6.2	1186	22	AA105293	Human genome-deriv
C 45	34.6	6.2	1186	24	AB512641	

ALIGNMENTS

Science / Confirmation



1

DNA encoding a human progesterone receptor complex p23-like protein.

Human progesterone receptor complex p23-like protein; PR23P, neuro|logical disorder; antagonist; nonreproductive disorder.

Immunological disorder; neoplastic disorder; ss

Homo sapiens

W09919483-A1.

22-APR-1999

09-0000-1000

100

11 OCT 1951

(INCY-) INCYT

Corley NC, 5

WPI; 1999-302

F-100B; 00102

Human progest

Sequence Comparison

Claim 7; Fig 1A-B; 67pp; English.

The present sequence encodes a human progesterone receptor complex PR23-like protein (PR23P). PR23P is used to treat neurological disorders. Antagonists of PR23P are useful for treating reproductive, immunological or neoplastic disorders. Probes and primers based on the PR23P polynucleotides can be used for diagnosis, detection and screening of homologues, and amplification of PR23P genes. Antisense PR23P polynucleotides can be used to decrease or inhibit expression of PR23P.

SQ Sequence 559 BP; 140 A; 114 C; 165 G; 140 T; 0 other;

Query Match 100.0%; Score 559; DB 20; Length 559;

Best Local Similarity 100.0%; Pred. No. 4.6e-171;

Matches 559; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCGCAATGGACGCGACGACCCCGGACCTTGTGTACGACAGCCCATGTATGTGTCA 60
DB 1 CCGCAATGGACGCGACGACCCCGGACCTTGTGTACGACAGCCCATGTATGTGTCA 60
QY 61 TGGAGTTTGTGTGAGGACGACGACGATGTCACGTCATATGAGGATACCGCATG 120
DB 61 TGGAGTTTGTGTGAGGACGACGACGATGTCACGTCATATGAGGATACCGCATG 120
QY 121 TGTTCAGCTGCAAGATGCGATGAGTGTGATGATGATGATGATGATGATGATG 180
DB 121 TGTTCAGCTGCAAGATGCGATGAGTGTGATGATGATGATGATGATGATGATG 180
QY 181 AAGTGAATCCCAAGAGATCCCAAGATGAGGCTCTCCGCTCTATTAATGTTTGTGA 240
DB 181 AAGTGAATCCCAAGAGATCCCAAGATGAGGCTCTCCGCTCTATTAATGTTTGTGA 240
QY 241 GAAATGGAAGAAAGAGTGGCGGCGGCTTACCAAGAGAGATATCAAGCAGTGT 300
DB 241 GAAATGGAAGAAAGAGTGGCGGCGGCTTACCAAGAGAGATATCAAGCAGTGT 300
QY 301 GCGTGTCTGTGACTTGTGATGAGAGAGTGGAGAGGAGATGAAGATGAGAGTGG 360
DB 301 GCGTGTCTGTGACTTGTGATGAGAGAGTGGAGAGGAGATGAAGATGAGAGTGG 360
QY 361 CTTGATGGAACATTAAGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGG 420
DB 361 CTTGATGGAACATTAAGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGG 420
QY 421 CCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 421 CCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 481 CTGTGACGCAAGCTGGAGAGGAGCTGTGCTATTTTCCAGTTGTTAGAAAGCTAG 540
DB 481 CTGTGACGCAAGCTGGAGAGGAGCTGTGCTATTTTCCAGTTGTTAGAAAGCTAG 540
QY 541 GCGTAGGCGCTTGTGACGG 559
DB 541 GCGTAGGCGCTTGTGACGG 559
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RESULT 2

AA158712 standard; cDNA; 1006 BP.

AA158712;

22-OCT-2001 (first entry)

Human polynucleotide SEQ ID NO 915.

Human: nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

leukaemia; ss.
Homo sapiens.
WO200153312-A1.
26-JUL-2001.
26-DEC-2000; 2000WO-US34263.
21-JAN-2000; 2000US-0488725.
23-APR-2000; 2000US-052317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
(HYSE-) HYSEQ INC.
Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang
Wang J, Wang Z, Wehman R, Xu C, Xue AJ, Yang Y, Zhang J;
Zhou QA, Zhou P, Goodrich R, Drmanac RT;
WPI; 2001-442253/47.
P-PSDB; AAM39556.
Novel nucleic acids and polypeptides, useful for treating disorders
such as central nervous system injuries -
Claim 1; SEQ ID NO 915; 10078pp; English.

The invention relates to human nucleic acids (AA15798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: immune system suppression, CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukaemia and CC C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed specification.

SQ Sequence 1006 BP; 235 A; 244 C; 265 G; 262 T; 0 other;

Query Match 98.3%; Score 549.4; DB 22; Length 1006;

Best Local Similarity 99.8%; Pred. No. 8.4e-168;

Matches 550; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CCGCAATGGACGCGACGACCCCGGACCTTGTGTACGACAGCCCATGTATGTGTCA 60
DB 360 CCGCAATGGACGCGACGACCCCGGACCTTGTGTACGACAGCCCATGTATGTGTCA 419
QY 61 TGGAGTTTGTGTGAGGACGACGACGATGTCACGTCATATGAGGATACCGCATG 120
DB 420 TGGAGTTTGTGTGAGGACGACGACGATGTCACGTCATATGAGGATACCGCATG 479
QY 121 TGTTCAGCTGCAAGATGCGATGAGTGTGATGATGATGATGATGATGATGATG 180
DB 480 TGTTCAGCTGCAAGATGCGATGAGTGTGATGATGATGATGATGATGATGATG 539
QY 181 AAGTGAATCCCAAGAGATCCCAAGATGAGGCTCTCCGCTCTATTAATGTTTGTGA 240
DB 540 AAGTGAATCCCAAGAGATCCCAAGATGAGGCTCTCCGCTCTATTAATGTTTGTGA 599
QY 241 GAAATGGAAGAAAGAGTGGCGGCGGCTTACCAAGAGAGATATCAAGCAGTGT 300
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